

Sequence Listing

<110> LG Life Sciences, Ltd.

<120> Gene families associated with stomach cancer

<130> PC03015-LG

<150> US 60/402,904

<151> 2002-08-14

<150> US 60/404,408

<151> 2002-08-20

<150> US 60/405,304

<151> 2002-08-23

<150> US 60/421,582

<151> 2002-10-28

<160> 22

<170> KopatentIn 1.71

<210> 1

<211> 1272

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (131)..(859)

<223> Gene LBFL301, Clone AD12

<400> 1

ggcgcgcggg tgaaaggcgc attgatgcag cctgcggcgg cctcggagcg cggcggagcc 60

agacgctgac cacgttcctc tcctcgggtct cctccgcctc cagctccgcg ctgcccggca 120

gccgggagcc atg cga ccc cag ggc ccc gcc gcc tcc ccg cag cgg ctc cgc 172

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg

Sequence Listing

1	5	10	
ggc ctc ctg ctg ctc ctg ctg ctg cag ctg ccc gcg ccg tcg agc gcc			220
Gly Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala			
15	20	25	30
tct gag atc ccc aag ggg aag caa aag gcg cag ctc cgg cag agg gag			268
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu			
35	40	45	
gtg gtg gac ctg tat aat gga atg tgc tta caa ggg cca gca gga gtg			316
Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val			
50	55	60	
cct ggt cga gac ggg agc cct ggg gcc aat ggc att ccg ggt aca cct			364
Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro			
65	70	75	
ggg atc cca ggt cgg gat gga ttc aaa gga gaa aag ggg gaa tgt ctg			412
Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu			
80	85	90	
agg gaa agc ttt gag gag tcc tgg aca ccc aac tac aag cag tgt tca			460
Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser			
95	100	105	110
tgg agt tca ttg aat tat ggc ata gat ctt ggg aaa att gcg gag tgt			508
Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys			
115	120	125	
aca ttt aca aag atg cgt tca aat agt gct cta aga gtt ttg ttc agt			556
Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser			
130	135	140	
ggc tca ctt cgg cta aaa tgc aga aat gca tgc tgt cag cgt tgg tat			604
Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr			
145	150	155	
ttc aca ttc aat gga gct gaa tgt tca gga cct ctt ccc att gaa gct			652
Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala			

Sequence Listing

160	165	170	
ata att tat ttg gac caa gga agc cct gaa atg aat tca aca att aat			700
Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn			
175	180	185	190
att cat cgc act tct tct gtg gaa gga ctt tgt gaa gga att ggt gct			748
Ile His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala			
	195	200	205
gga tta gtg gat gtt gct atc tgg gtt ggc act tgt tca gat tac cca			796
Gly Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro			
	210	215	220
aaa gga gat gct tct act gga tgg aat tca gtt tct cgc atc att att			844
Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile			
	225	230	235
gaa gaa cta cca aaa t aaatgcttta attttcattt gctacctctt tttttattat			900
Glu Glu Leu Pro Lys			
	240		
gccttggaat ggttcactta aatgacattt taaataagtt tatgtataca tctgaatgaa			960
aagcaaagct aaatatgttt acagaccaaa gtgtgatttc acactgtttt taaatctagc			1020
attattcatt ttgcttcaat caaaagtggg ttcaatattt tttttagttg gttagaatac			1080
tttcttcata gtcacattct ctcaacctat aatttggaat attggtgtgg tcttttgttt			1140
tttctcttag tatagcattt ttaaaaaaat ataaaagcta ccaatctttg tacaatttgt			1200
aaatgttaag aatttttttt atatctgtta aataaaaatt atttccaaca accttaaaaa			1260
aaaaaaaaaa aa			1272

<210> 2

<211> 243

<212> PRT

Sequence Listing

<213> Homo sapiens

<400> 2

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Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
  1             5             10             15

Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
      20             25             30

Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val
      35             40             45

Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
      50             55             60

Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly Ile
      65             70             75             80

Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu
      85             90             95

Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser
      100            105            110

Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe
      115            120            125

Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser
      130            135            140

Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr
      145            150            155            160

Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile
      165            170            175

Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His
      180            185            190

Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu

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Sequence Listing

195 200 205
 Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly
 210 215 220

Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 225 230 235 240

Leu Pro Lys

<210> 3
 <211> 1355
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (174)..(584)
 <223> Gene LBFL301, Clone CH4

<400> 3
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 cgcattgatg cagcctgcgg cggcctcgga gcgcggcgga gccagacgct gaccacgttc 120
 ctctctcgg tctctccgc ctccagctcc gcgctgccg gcagccggga gcc 173
 atg cga ccc cag ggc ccc gcc gcc tcc ccg cag cgg ctc cgc ggc ctc 221
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
 1 5 10 15
 ctg ctg ctc ctg ctg ctg cag ctg ccc gcg ccg tcg agc gcc tct gag 269
 Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
 20 25 30
 atc ccc aag ggg aag caa aag gcg cag ctc cgg cag agg gag gtg gtg 317
 Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val

Sequence Listing

35	40	45	
gac ctg tat aat gga atg tgc tta caa ggg cca gca gga gtg cct ggt Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly 50	55	60	365
cga gac ggg agc cct ggg gcc aat ggc att ccg ggt aca cct ggg atc Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly Ile 65	70	75	413
cca ggt cgg gat gga ttc aaa gga gaa aag ggg gaa tgt ctg agg gaa Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu 85	90	95	461
agc ttt gag gag tcc tgg aca ccc aac tac aag cag tgt tca tgg agt Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser 100	105	110	509
tca ttg aat tat ggc ata gat ctt ggg aaa att gcg aaa cac gtc aag Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Lys His Val Lys 115	120	125	557
agt caa tac gaa tgg aca gaa cta gtc tagaat gagtgtacat ttacaaagat Ser Gln Tyr Glu Trp Thr Glu Leu Val 130	135		610
gcgttcaa at agtgctctaa gagttttggt cagtggctca cttcggctaa aatgcagaaa			670
tgcatgctgt cagcgttggt atttcacatt caatggagct gaatgttcag gacctcttcc			730
cattgaagct ataatttatt tggaccaagg aagccctgaa atgaattcaa caattaatat			790
tcatcgact tcttctgtgg aaggactttg tgaaggaatt ggtgctggat tagtggatgt			850
tgctatctgg gttggcactt gttcagatta cccaaaagga gatgcttcta ctggatggaa			910
ttcagtttct cgcatacatta ttgaagaact accaaaataa atgctttaat tttcatttgc			970
tacctctttt tttattatgc cttggaatgg ttcacttaaa tgacatttta aataagttaa			1030

Sequence Listing

tgtatacatc tgaatgaaaa gcaaagctaa atatgtttac agaccaaagt gtgatttcac 1090

actgttttta aatctagcat tattcathtt gtttcaatca aaagtgggtt caatattttt 1150

tttagttggt tagaatactt tcttcatagt cacattctct caacctataa tttggaatat 1210

tgttgtgggc ttttgttttt tctcttagta tagcattttt aaaaaaatat aaaagctacc 1270

aatctttgta caatttgtaa atgttaagaa ttttttttat atctgttaaa taaaaattat 1330

ttccaacaaa aaaaaaaaaa aaaaa 1355

<210> 4

<211> 137

<212> PRT

<213> Homo sapiens

<400> 4

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
1 5 10 15

Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
20 25 30

Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val
35 40 45

Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
50 55 60

Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly Ile
65 70 75 80

Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu
85 90 95

Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser
100 105 110

Sequence Listing

Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Lys His Val Lys
 115 120 125

Ser Gln Tyr Glu Trp Thr Glu Leu Val
 130 135

<210> 5
 <211> 2500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (38)..(892)
 <223> Clone LBFL304, ORF1

<400> 5
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 Met Leu Glu Ile Lys
 1 5

atg gag gaa gct atg acc tac aca gag gac agt tat ggg atg gat ggg 100
 Met Glu Glu Ala Met Thr Tyr Thr Glu Asp Ser Tyr Gly Met Asp Gly
 10 15 20

aag gtt aat cag ccc cgt ctc act gca gac atc aac tgg caa ggc cta 148
 Lys Val Asn Gln Pro Arg Leu Thr Ala Asp Ile Asn Trp Gln Gly Leu
 25 30 35

gag gag cta cac agt gtg aat gaa aac atc tat gag tac aga caa aac 196
 Glu Glu Leu His Ser Val Asn Glu Asn Ile Tyr Glu Tyr Arg Gln Asn
 40 45 50

tac aga ctt agt ctg gtg gac tgg act aat tac ttg aag gat tta gat 244
 Tyr Arg Leu Ser Leu Val Asp Trp Thr Asn Tyr Leu Lys Asp Leu Asp
 55 60 65

aga gta ttt gca ctg ctg aag agt cac tat gag caa aat aaa aca aat 292

Sequence Listing

Arg Val Phe Ala Leu Leu Lys Ser His Tyr Glu Gln Asn Lys Thr Asn			
70	75	80	85
aag act caa act gct caa agt gac ggg ttc ttg gtt gtc tct gct gag			340
Lys Thr Gln Thr Ala Gln Ser Asp Gly Phe Leu Val Val Ser Ala Glu			
	90	95	100
cac gct gtg tca atg gag atg gcc tct gct gac tca gat gaa gac cca			388
His Ala Val Ser Met Glu Met Ala Ser Ala Asp Ser Asp Glu Asp Pro			
	105	110	115
agg cat aag gtt ggg aaa aca cct cat ttg acc ttg cca gct gac ctt			436
Arg His Lys Val Gly Lys Thr Pro His Leu Thr Leu Pro Ala Asp Leu			
	120	125	130
caa acc ctg cat ttg aac cga cca aca tta agt cca gag agt aaa ctt			484
Gln Thr Leu His Leu Asn Arg Pro Thr Leu Ser Pro Glu Ser Lys Leu			
	135	140	145
gaa tgg aat aac gac att cca gaa gtt aat cat ttg aat tct gaa cac			532
Glu Trp Asn Asn Asp Ile Pro Glu Val Asn His Leu Asn Ser Glu His			
	150	155	160
tgg aga aaa acc gaa aaa tgg acg ggg cat gaa gag act aat cat ctg			580
Trp Arg Lys Thr Glu Lys Trp Thr Gly His Glu Glu Thr Asn His Leu			
	170	175	180
gaa acc gat ttc agt ggc gat ggc atg aca gag cta gag ctc ggg ccc			628
Glu Thr Asp Phe Ser Gly Asp Gly Met Thr Glu Leu Glu Leu Gly Pro			
	185	190	195
agc ccc agg ctg cag ccc att cgc agg cac ccg aaa gaa ctt ccc cag			676
Ser Pro Arg Leu Gln Pro Ile Arg Arg His Pro Lys Glu Leu Pro Gln			
	200	205	210
tat ggt ggt cct gga aag gac att ttt gaa gat caa cta tat ctt cct			724
Tyr Gly Gly Pro Gly Lys Asp Ile Phe Glu Asp Gln Leu Tyr Leu Pro			
	215	220	225
gtg cat tcc gat gga att tca gtt cat cag atg ttc acc atg gcc acc			772

Sequence Listing

Val His Ser Asp Gly Ile Ser Val His Gln Met Phe Thr Met Ala Thr			
230	235	240	245
gca gaa cac cga agt aat tcc agc ata gcg ggg aag atg ttg acc aag			820
Ala Glu His Arg Ser Asn Ser Ser Ile Ala Gly Lys Met Leu Thr Lys			
250	255	260	
gtg gag aag aat cac gaa aag gag aag tca cag cac cta gaa ggc agc			868
Val Glu Lys Asn His Glu Lys Glu Lys Ser Gln His Leu Glu Gly Ser			
265	270	275	
gcc tcc tct tca ctc tcc tct gat tagatgaa actgttacct taccctaaac			920
Ala Ser Ser Ser Leu Ser Ser Asp			
280	285		
acagtatttc tttttaactt ttttatttgt aaactaataa aggtaatcac agccaccaac			980
attccaagct accctgggta cctttgtgca gtagaagcta gtgagcatgt gagcaagcgg			1040
tgtgcacacg gagactcatc gttataattt actatctgcc aagagtagaa agaaaggctg			1100
gggatatttg gggtggcttg gttttgattt tttgcttggt tgtttgtttt gtactaaaac			1160
agtattatct tttgaatata gtagggacat aagtatatatac atgttatcca atcaagatgg			1220
ctagaatggt gcctttctga gtgtctaaaa cttgacaccc ctggtaaatc tttcaacaca			1280
cttccactgc ctgcgtaatg aagttttgat tcatttttaa ccaactggaat ttttcaatgc			1340
cgtcattttc agttagatga ttttgcaactt tgagattaaa atgccatgtc tatttgatta			1400
gtcttatttt tttattttta caggcttatc agtctcactg ttggctgtca ttgtgacaaa			1460
gtcaaataaa cccccaagga cgacacacag tatggatcac atattgtttg acattaagct			1520
tttgccagaa aatgttgcat gtgttttacc tcgacttgct aaaatcgatt agcagaaagg			1580
catggctaata aatgttggtg gtgaaaataa ataaataagt aaacaaaatg aagattgcct			1640
gctctctctg tgcctagcct caaagcgttc atcatatc atacctttaa gattgctata			1700

Sequence Listing

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ttttgggtta ttttcttgac aggagaaaaa gatctaaaga tcttttattt tcatcttttt 1760
tggttttcctt ggcatgacta agaagcttaa atgttgataa aatatgacta gttttgaatt 1820
tacaccaaga acttctcaat aaaagaaaat catgaatgct ccacaatttc aacataccac 1880
aagagaagtt aatttcttaa cattgtgttc tatgattatt tgtaagacct tcaccaagtt 1940
ctgatatcctt ttaaagacat agttcaaaat tgcttttgaa aatctgtatt cttgaaaata 2000
tccttgttgt gtattaggtt tttaaatacc agctaaagga ttacctcact gagtcatcag 2060
taccctccta ttcagctccc caagatgatg tgtttttgct taccctaaga gaggttttct 2120
tcttattttt agataattca agtgcttaga taaattatgt tttctttaag tgfttatggt 2180
aaactctttt aaagaaaatt taatatgtta tagctgaatc tttttggtaa ctttaaactt 2240
ttatcataga ctctgtacat atgttcaaat tagctgcttg cctgatgtgt gtatcatcgg 2300
tgggatgaca gaacaaacat atttatgac atgaataatg tgctttgtaa aaagatttca 2360
agttattagg aagcatactc tgttttttaa tcatgtataa tattccatga tacttttata 2420
gaacaattct ggcttcagga aagtctagaa gcaatatttc ttcaaataaa aggtgtttaa 2480
actttaaaaa aaaaaaaaaa 2500

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<210> 6

<211> 285

<212> PRT

<213> Homo sapiens

<400> 6

Met Leu Glu Ile Lys Met Glu Glu Ala Met Thr Tyr Thr Glu Asp Ser

1

5

10

15

Tyr Gly Met Asp Gly Lys Val Asn Gln Pro Arg Leu Thr Ala Asp Ile

Sequence Listing

20	25	30
Asn Trp Gln Gly Leu Glu Glu Leu His Ser Val Asn Glu Asn Ile Tyr		
35	40	45
Glu Tyr Arg Gln Asn Tyr Arg Leu Ser Leu Val Asp Trp Thr Asn Tyr		
50	55	60
Leu Lys Asp Leu Asp Arg Val Phe Ala Leu Leu Lys Ser His Tyr Glu		
65	70	75
Gln Asn Lys Thr Asn Lys Thr Gln Thr Ala Gln Ser Asp Gly Phe Leu		
85	90	95
Val Val Ser Ala Glu His Ala Val Ser Met Glu Met Ala Ser Ala Asp		
100	105	110
Ser Asp Glu Asp Pro Arg His Lys Val Gly Lys Thr Pro His Leu Thr		
115	120	125
Leu Pro Ala Asp Leu Gln Thr Leu His Leu Asn Arg Pro Thr Leu Ser		
130	135	140
Pro Glu Ser Lys Leu Glu Trp Asn Asn Asp Ile Pro Glu Val Asn His		
145	150	155
Leu Asn Ser Glu His Trp Arg Lys Thr Glu Lys Trp Thr Gly His Glu		
165	170	175
Glu Thr Asn His Leu Glu Thr Asp Phe Ser Gly Asp Gly Met Thr Glu		
180	185	190
Leu Glu Leu Gly Pro Ser Pro Arg Leu Gln Pro Ile Arg Arg His Pro		
195	200	205
Lys Glu Leu Pro Gln Tyr Gly Gly Pro Gly Lys Asp Ile Phe Glu Asp		
210	215	220
Gln Leu Tyr Leu Pro Val His Ser Asp Gly Ile Ser Val His Gln Met		
225	230	235
		240

Sequence Listing

Phe Thr Met Ala Thr Ala Glu His Arg Ser Asn Ser Ser Ile Ala Gly
 245 250 255

Lys Met Leu Thr Lys Val Glu Lys Asn His Glu Lys Glu Lys Ser Gln
 260 265 270

His Leu Glu Gly Ser Ala Ser Ser Ser Leu Ser Ser Asp
 275 280 285

<210> 7
 <211> 2500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53)..(892)
 <223> Clone LBFL304, ORF2

<400> 7
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atg gag gaa gct atg acc tac aca gag gac agt tat ggg atg gat ggg 100
 Met Glu Glu Ala Met Thr Tyr Thr Glu Asp Ser Tyr Gly Met Asp Gly
 1 5 10 15

aag gtt aat cag ccc cgt ctc act gca gac atc aac tgg caa ggc cta 148
 Lys Val Asn Gln Pro Arg Leu Thr Ala Asp Ile Asn Trp Gln Gly Leu
 20 25 30

gag gag cta cac agt gtg aat gaa aac atc tat gag tac aga caa aac 196
 Glu Glu Leu His Ser Val Asn Glu Asn Ile Tyr Glu Tyr Arg Gln Asn
 35 40 45

tac aga ctt agt ctg gtg gac tgg act aat tac ttg aag gat tta gat 244
 Tyr Arg Leu Ser Leu Val Asp Trp Thr Asn Tyr Leu Lys Asp Leu Asp
 50 55 60

Sequence Listing

aga gta ttt gca ctg ctg aag agt cac tat gag caa aat' aaa aca aat	292
Arg Val Phe Ala Leu Leu Lys Ser His Tyr Glu Gln Asn Lys Thr Asn	
65 70 75 80	
aag act caa act gct caa agt gac ggg ttc ttg gtt gtc tct gct gag	340
Lys Thr Gln Thr Ala Gln Ser Asp Gly Phe Leu Val Val Ser Ala Glu	
85 90 95	
cac gct gtg tca atg gag atg gcc tct gct gac tca gat gaa gac cca	388
His Ala Val Ser Met Glu Met Ala Ser Ala Asp Ser Asp Glu Asp Pro	
100 105 110	
agg cat aag gtt ggg aaa aca cct cat ttg acc ttg cca gct gac ctt	436
Arg His Lys Val Gly Lys Thr Pro His Leu Thr Leu Pro Ala Asp Leu	
115 120 125	
caa acc ctg cat ttg aac cga cca aca tta agt cca gag agt aaa ctt	484
Gln Thr Leu His Leu Asn Arg Pro Thr Leu Ser Pro Glu Ser Lys Leu	
130 135 140	
gaa tgg aat aac gac att cca gaa gtt aat cat ttg aat tct gaa cac	532
Glu Trp Asn Asn Asp Ile Pro Glu Val Asn His Leu Asn Ser Glu His	
145 150 155 160	
tgg aga aaa acc gaa aaa tgg acg ggg cat gaa gag act aat cat ctg	580
Trp Arg Lys Thr Glu Lys Trp Thr Gly His Glu Glu Thr Asn His Leu	
165 170 175	
gaa acc gat ttc agt ggc gat ggc atg aca gag cta gag ctc ggg ccc	628
Glu Thr Asp Phe Ser Gly Asp Gly Met Thr Glu Leu Glu Leu Gly Pro	
180 185 190	
agc ccc agg ctg cag ccc att cgc agg cac ccg aaa gaa ctt ccc cag	676
Ser Pro Arg Leu Gln Pro Ile Arg Arg His Pro Lys Glu Leu Pro Gln	
195 200 205	
tat ggt ggt cct gga aag gac att ttt gaa gat caa cta tat ctt cct	724
Tyr Gly Gly Pro Gly Lys Asp Ile Phe Glu Asp Gln Leu Tyr Leu Pro	
210 215 220	

Sequence Listing

gtg cat tcc gat gga att tca gtt cat cag atg ttc acc atg gcc acc	772
Val His Ser Asp Gly Ile Ser Val His Gln Met Phe Thr Met Ala Thr	
225 230 235 240	
 gca gaa cac cga agt aat tcc agc ata gcg ggg aag atg ttg acc aag	820
Ala Glu His Arg Ser Asn Ser Ser Ile Ala Gly Lys Met Leu Thr Lys	
245 250 255	
 gtg gag aag aat cac gaa aag gag aag tca cag cac cta gaa ggc agc	868
Val Glu Lys Asn His Glu Lys Glu Lys Ser Gln His Leu Glu Gly Ser	
260 265 270	
 gcc tcc tct tca ctc tcc tct gat tagatgaa actgttacct taccctaaac	920
Ala Ser Ser Ser Leu Ser Ser Asp	
275 280 .	
 acagtatttc tttttaactt ttttatttgt aaactaataa aggtaatcac agccaccaac	980
 attccaagct accctgggta cctttgtgca gtagaagcta gtgagcatgt gagcaagcgg	1040
 tgtgcacacg gagactcatc gttataattt actatctgcc aagagtagaa agaaaggctg	1100
 gggatatttg ggttggttg gttttgattt tttgcttggt tgtttgtttt gtactaaaac	1160
 agtattatct tttgaatatc gtagggacat aagtatatac atgttatcca atcaagatgg	1220
 ctagaatggg gcctttctga gtgtctaaaa cttgacaccc ctggtaaatc tttcaacaca	1280
 cttcactgc ctgcgtaatg aagttttgat tcatttttaa ccaactggaat ttttcaatgc	1340
 cgtcattttc agttagatga ttttgcaactt tgagattaaa atgccatgtc tatttgatta	1400
 gtcttatttt tttattttta caggcttacc agtctcactg ttggctgtca ttgtgacaaa	1460
 gtcaaataaa cccccaagga cgacacacag tatggatcac atattgtttg acattaagct	1520
 tttgccagaa aatggtgcat gtgttttacc tcgacttgct aaaatcgatt agcagaaaagg	1580
 catgggcta atgtttggtg gtgaaaataa ataaataagt aaacaaaatg aagattgcct	1640

Sequence Listing

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gctctctctg tgcctagcct caaagcggtc atcatcacatc atacctttaa gattgctata      1700
ttttgggtta ttttcttgac aggagaaaaa gatctaaaga tcttttattt tcatcttttt      1760
tggttttctt ggcattgacta agaagcttaa atgttgataa aatatgacta gttttgaatt      1820
tacaccaaga acttctcaat aaaagaaaat catgaatgct ccacaatttc aacataccac      1880
aagagaagtt aatttcttaa cattgtgttc tatgattatt tgtaagacct tcaccaagtt      1940
ctgatatctt ttaaagacat agttcaaaaat tgcttttgaa aatctgtatt ctgaaaata      2000
tccttgttgt gtattagggt tttaaatacc agctaaagga ttacctcact gagtcacag      2060
taccctccta ttcagctccc caagatgatg tgtttttgct taccctaaga gaggttttct      2120
tcttattttt agataattca agtgcttaga taaattatgt tttctttaag tgtttatggt      2180
aaactctttt aaagaaaatt taatatgtta tagctgaatc tttttggtta ctttaaactc      2240
ttatcataga ctctgtacat atgttcaaat tagctgcttg cctgatgtgt gtatcatcgg      2300
tgggatgaca gaacaaacat atttatgac atgaataatg tgctttgtaa aaagatttca      2360
agttattagg aagcatactc tgttttttta tcatgtataa tattccatga tacttttata      2420
gaacaattct ggcttcagga aagtctagaa gcaatatttc ttcaaataaa aggtgtttta      2480
actttaaaaa aaaaaaaaaa                                     2500

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<210> 8

<211> 280

<212> PRT

<213> Homo sapiens

<400> 8

Met Glu Glu Ala Met Thr Tyr Thr Glu Asp Ser Tyr Gly Met Asp Gly

1

5

10

15

Sequence Listing

Lys Val Asn Gln Pro Arg Leu Thr Ala Asp Ile Asn Trp Gln Gly Leu
 20 25 30

Glu Glu Leu His Ser Val Asn Glu Asn Ile Tyr Glu Tyr Arg Gln Asn
 35 40 45

Tyr Arg Leu Ser Leu Val Asp Trp Thr Asn Tyr Leu Lys Asp Leu Asp
 50 55 60

Arg Val Phe Ala Leu Leu Lys Ser His Tyr Glu Gln Asn Lys Thr Asn
 65 70 75 80

Lys Thr Gln Thr Ala Gln Ser Asp Gly Phe Leu Val Val Ser Ala Glu
 85 90 95

His Ala Val Ser Met Glu Met Ala Ser Ala Asp Ser Asp Glu Asp Pro
 100 105 110

Arg His Lys Val Gly Lys Thr Pro His Leu Thr Leu Pro Ala Asp Leu
 115 120 125

Gln Thr Leu His Leu Asn Arg Pro Thr Leu Ser Pro Glu Ser Lys Leu
 130 135 140

Glu Trp Asn Asn Asp Ile Pro Glu Val Asn His Leu Asn Ser Glu His
 145 150 155 160

Trp Arg Lys Thr Glu Lys Trp Thr Gly His Glu Glu Thr Asn His Leu
 165 170 175

Glu Thr Asp Phe Ser Gly Asp Gly Met Thr Glu Leu Glu Leu Gly Pro
 180 185 190

Ser Pro Arg Leu Gln Pro Ile Arg Arg His Pro Lys Glu Leu Pro Gln
 195 200 205

Tyr Gly Gly Pro Gly Lys Asp Ile Phe Glu Asp Gln Leu Tyr Leu Pro
 210 215 220

Sequence Listing

Val His Ser Asp Gly Ile Ser Val His Gln Met Phe Thr Met Ala Thr
 225 230 235 240

Ala Glu His Arg Ser Asn Ser Ser Ile Ala Gly Lys Met Leu Thr Lys
 245 250 255

Val Glu Lys Asn His Glu Lys Glu Lys Ser Gln His Leu Glu Gly Ser
 260 265 270

Ala Ser Ser Ser Leu Ser Ser Asp
 275 280

<210> 9
 <211> 2500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (65)..(892)
 <223> Clone LBFL304, ORF3

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 agct atg acc tac aca gag gac agt tat ggg atg gat ggg aag gtt 106
 Met Thr Tyr Thr Glu Asp Ser Tyr Gly Met Asp Gly Lys Val
 1 5 10

 aat cag ccc cgt ctc act gca gac atc aac tgg caa ggc cta gag gag 154
 Asn Gln Pro Arg Leu Thr Ala Asp Ile Asn Trp Gln Gly Leu Glu Glu
 15 20 25 30

 cta cac agt gtg aat gaa aac atc tat gag tac aga caa aac tac aga 202
 Leu His Ser Val Asn Glu Asn Ile Tyr Glu Tyr Arg Gln Asn Tyr Arg
 35 40 45

 ctt agt ctg gtg gac tgg act aat tac ttg aag gat tta gat aga gta 250

Sequence Listing

Leu Ser Leu Val Asp Trp Thr Asn Tyr Leu Lys Asp Leu Asp Arg Val	
50 55 60	
ttt gca ctg ctg aag agt cac tat gag caa aat aaa aca aat aag act	298
Phe Ala Leu Leu Lys Ser His Tyr Glu Gln Asn Lys Thr Asn Lys Thr	
65 70 75	
caa act gct caa agt gac ggg ttc ttg gtt gtc tct gct gag cac gct	346
Gln Thr Ala Gln Ser Asp Gly Phe Leu Val Val Ser Ala Glu His Ala	
80 85 90	
gtg tca atg gag atg gcc tct gct gac tca gat gaa gac cca agg cat	394
Val Ser Met Glu Met Ala Ser Ala Asp Ser Asp Glu Asp Pro Arg His	
95 100 105 110	
aag gtt ggg aaa aca cct cat ttg acc ttg cca gct gac ctt caa acc	442
Lys Val Gly Lys Thr Pro His Leu Thr Leu Pro Ala Asp Leu Gln Thr	
115 120 125	
ctg cat ttg aac cga cca aca tta agt cca gag agt aaa ctt gaa tgg	490
Leu His Leu Asn Arg Pro Thr Leu Ser Pro Glu Ser Lys Leu Glu Trp	
130 135 140	
aat aac gac att cca gaa gtt aat cat ttg aat tct gaa cac tgg aga	538
Asn Asn Asp Ile Pro Glu Val Asn His Leu Asn Ser Glu His Trp Arg	
145 150 155	
aaa acc gaa aaa tgg acg ggg cat gaa gag act aat cat ctg gaa acc	586
Lys Thr Glu Lys Trp Thr Gly His Glu Glu Thr Asn His Leu Glu Thr	
160 165 170	
gat ttc agt ggc gat ggc atg aca gag cta gag ctc ggg ccc agc ccc	634
Asp Phe Ser Gly Asp Gly Met Thr Glu Leu Glu Leu Gly Pro Ser Pro	
175 180 185 190	
agg ctg cag ccc att cgc agg cac ccg aaa gaa ctt ccc cag tat ggt	682
Arg Leu Gln Pro Ile Arg Arg His Pro Lys Glu Leu Pro Gln Tyr Gly	
195 200 205	
ggt cct gga aag gac att ttt gaa gat caa cta tat ctt cct gtg cat	730

Sequence Listing

Gly Pro Gly Lys Asp Ile Phe Glu Asp Gln Leu Tyr Leu Pro Val His	210	215	220	
tcc gat gga att tca gtt cat cag atg ttc acc atg gcc acc gca gaa				778
Ser Asp Gly Ile Ser Val His Gln Met Phe Thr Met Ala Thr Ala Glu	225	230	235	
cac cga agt aat tcc agc ata gcg ggg aag atg ttg acc aag gtg gag				826
His Arg Ser Asn Ser Ser Ile Ala Gly Lys Met Leu Thr Lys Val Glu	240	245	250	
aag aat cac gaa aag gag aag tca cag cac cta gaa ggc agc gcc tcc				874
Lys Asn His Glu Lys Glu Lys Ser Gln His Leu Glu Gly Ser Ala Ser	255	260	265	270
tct tca ctc tcc tct gat tagatgaa actgttacct taccctaaac acagtatttc				930
Ser Ser Leu Ser Ser Asp	275			
tttttaactt ttttatgtgt aaactaataa aggtaatcac agccaccaac attccaagct				990
accctgggta cctttgtgca gtagaagcta gtgagcatgt gagcaagcgg tgtgcacacg				1050
gagactcatc gttataatct actatctgcc aagagtagaa agaaaggctg gggatatttg				1110
ggttggtctg gttttgatct tttgcttggt tgtttgtttt gtactaaaac agtattatct				1170
tttgaatatc gtagggacat aagtatatac atgttatcca atcaagatgg ctagaatggt				1230
gcctttctga gtgtctaaaa cttgacaccc ctggtaaatc tttcaacaca cttccactgc				1290
ctgcgtaatg aagttttgat tcatttttaa ccaactggaat ttttcaatgc cgtcattttc				1350
agttagatga ttttgcaactt tgagattaaa atgccatgtc tatttgatta gtcttatttt				1410
tttattttta caggcttatac agtctcactg ttggctgtca ttgtgacaaa gtcaaataaa				1470
ccccaagga cgacacacag tatggatcac atattgtttg acattaagct tttgccagaa				1530
aatgttgcac gtgttttacc tcgacttgct aaaatcgatt agcagaaagg catggctaata				1590

Sequence Listing

aatgttggtg gtgaaaataa ataaataagt aaacaaaatg aagattgcct gctctctctg	1650
tgcctagcct caaagcggtc atcatacatc atacctttaa gattgctata ttttgggtta	1710
ttttcttgac aggagaaaaa gatctaaaga tcttttattt tcctcttttt tggttttctt	1770
ggcatgacta agaagcttaa atgttgataa aatatgacta gttttgaatt tacaccaaga	1830
acttctcaat aaaagaaaat catgaatgct ccacaatttc aacataccac aagagaagtt	1890
aattttctta cattgtgttc tatgattatt tgtaagacct tcaccaagtt ctgatattct	1950
ttaaagacat agttcaaaat tgcttttgaa aatctgtatt ctgaaaata tccttggtgt	2010
gtattaggtt tttaaatacc agctaaagga ttacctact gagtcacag taccctccta	2070
ttcagctccc caagatgatg tgtttttgct taccctaaga gaggttttct tcttattttt	2130
agataattca agtgcttaga taaattatgt tttctttaag tgtttatggt aaactctttt	2190
aaagaaaatt taatatgtta tagctgaatc tttttggtta ctttaaactt ttatcataga	2250
ctctgtacat atgttcaaat tagctgcttg cctgatgtgt gtatcatcgg tgggatgaca	2310
gaacaaacat atttatgatc atgaataatg tgctttgtaa aaagatttca agttattag	2370
aagcatactc tgttttttta tcattgtata tattccatga tacttttata gaacaattct	2430
ggcttcagga aagtctagaa gcaatatttc ttcaaataaa aggtgtttta actttaaaaa	2490
aaaaaaaaaa	2500

<210> 10

<211> 276

<212> PRT

<213> Homo sapiens

<400> 10

Sequence Listing

Met Thr Tyr Thr Glu Asp Ser Tyr Gly Met Asp Gly Lys Val Asn Gln
 1 5 10 15
 Pro Arg Leu Thr Ala Asp Ile Asn Trp Gln Gly Leu Glu Glu Leu His
 20 25 30
 Ser Val Asn Glu Asn Ile Tyr Glu Tyr Arg Gln Asn Tyr Arg Leu Ser
 35 40 45
 Leu Val Asp Trp Thr Asn Tyr Leu Lys Asp Leu Asp Arg Val Phe Ala
 50 55 60
 Leu Leu Lys Ser His Tyr Glu Gln Asn Lys Thr Asn Lys Thr Gln Thr
 65 70 75 80
 Ala Gln Ser Asp Gly Phe Leu Val Val Ser Ala Glu His Ala Val Ser
 85 90 95
 Met Glu Met Ala Ser Ala Asp Ser Asp Glu Asp Pro Arg His Lys Val
 100 105 110
 Gly Lys Thr Pro His Leu Thr Leu Pro Ala Asp Leu Gln Thr Leu His
 115 120 125
 Leu Asn Arg Pro Thr Leu Ser Pro Glu Ser Lys Leu Glu Trp Asn Asn
 130 135 140
 Asp Ile Pro Glu Val Asn His Leu Asn Ser Glu His Trp Arg Lys Thr
 145 150 155 160
 Glu Lys Trp Thr Gly His Glu Glu Thr Asn His Leu Glu Thr Asp Phe
 165 170 175
 Ser Gly Asp Gly Met Thr Glu Leu Glu Leu Gly Pro Ser Pro Arg Leu
 180 185 190
 Gln Pro Ile Arg Arg His Pro Lys Glu Leu Pro Gln Tyr Gly Gly Pro
 195 200 205
 Gly Lys Asp Ile Phe Glu Asp Gln Leu Tyr Leu Pro Val His Ser Asp

Sequence Listing

210	215	220	
Gly Ile Ser Val His Gln Met Phe Thr Met Ala Thr Ala Glu His Arg			
225	230	235	240
Ser Asn Ser Ser Ile Ala Gly Lys Met Leu Thr Lys Val Glu Lys Asn			
245	250	255	
His Glu Lys Glu Lys Ser Gln His Leu Glu Gly Ser Ala Ser Ser Ser			
260	265	270	
Leu Ser Ser Asp			
275			

<210> 11
 <211> 2500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (92)..(892)
 <223> Clone LBFL304, ORF4

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agctatgacc tacacagagg acagttatgg g	
atg gat ggg aag gtt	106
Met Asp Gly Lys Val	
1 5	
aat cag ccc cgt ctc act gca gac atc aac tgg caa ggc cta gag gag	154
Asn Gln Pro Arg Leu Thr Ala Asp Ile Asn Trp Gln Gly Leu Glu Glu	
10 15 20	
cta cac agt gtg aat gaa aac atc tat gag tac aga caa aac tac aga	202
Leu His Ser Val Asn Glu Asn Ile Tyr Glu Tyr Arg Gln Asn Tyr Arg	
25 30 35	

Sequence Listing

ctt agt ctg gtg gac tgg act aat tac ttg aag gat tta gat aga gta Leu Ser Leu Val Asp Trp Thr Asn Tyr Leu Lys Asp Leu Asp Arg Val	250
40 45 50	
ttt gca ctg ctg aag agt cac tat gag caa aat aaa aca aat aag act Phe Ala Leu Leu Lys Ser His Tyr Glu Gln Asn Lys Thr Asn Lys Thr	298
55 60 65	
caa act gct caa agt gac ggg ttc ttg gtt gtc tct gct gag cac gct Gln Thr Ala Gln Ser Asp Gly Phe Leu Val Val Ser Ala Glu His Ala	346
70 75 80 85	
gtg tca atg gag atg gcc tct gct gac tca gat gaa gac cca agg cat Val Ser Met Glu Met Ala Ser Ala Asp Ser Asp Glu Asp Pro Arg His	394
90 95 100	
aag gtt ggg aaa aca cct cat ttg acc ttg cca gct gac ctt caa acc Lys Val Gly Lys Thr Pro His Leu Thr Leu Pro Ala Asp Leu Gln Thr	442
105 110 115	
ctg cat ttg aac cga cca aca tta agt cca gag agt aaa ctt gaa tgg Leu His Leu Asn Arg Pro Thr Leu Ser Pro Glu Ser Lys Leu Glu Trp	490
120 125 130	
aat aac gac att cca gaa gtt aat cat ttg aat tct gaa cac tgg aga Asn Asn Asp Ile Pro Glu Val Asn His Leu Asn Ser Glu His Trp Arg	538
135 140 145	
aaa acc gaa aaa tgg acg ggg cat gaa gag act aat cat ctg gaa acc Lys Thr Glu Lys Trp Thr Gly His Glu Glu Thr Asn His Leu Glu Thr	586
150 155 160 165	
gat ttc agt ggc gat ggc atg acg gag cta gag ctc ggg ccc agc ccc Asp Phe Ser Gly Asp Gly Met Thr Glu Leu Glu Leu Gly Pro Ser Pro	634
170 175 180	
agg ctg cag ccc att cgc agg cac ccg aaa gaa ctt ccc cag tat ggt Arg Leu Gln Pro Ile Arg Arg His Pro Lys Glu Leu Pro Gln Tyr Gly	682
185 190 195	

Sequence Listing

ggt cct gga aag gac att ttt gaa gat caa cta tat ctt cct gtg cat	730
Gly Pro Gly Lys Asp Ile Phe Glu Asp Gln Leu Tyr Leu Pro Val His	
200 205 210	
tcc gat gga att tca gtt cat cag atg ttc acc atg gcc acc gca gaa	778
Ser Asp Gly Ile Ser Val His Gln Met Phe Thr Met Ala Thr Ala Glu	
215 220 225	
cac cga agt aat tcc agc ata gcg ggg aag atg ttg acc aag gtg gag	826
His Arg Ser Asn Ser Ser Ile Ala Gly Lys Met Leu Thr Lys Val Glu	
230 235 240 245	
aag aat cac gaa aag gag aag tca cag cac cta gaa ggc agc gcc tcc	874
Lys Asn His Glu Lys Glu Lys Ser Gln His Leu Glu Gly Ser Ala Ser	
250 255 260	
tct tca ctc tcc tct gat tagatgaa actgttacct taccctaaac acagtatttc	930
Ser Ser Leu Ser Ser Asp	
265	
tttttaactt ttttatttgt aaactaataa aggtaatcac agccaccaac attccaagct	990
accctgggta cctttgtgca gtagaagcta gtgagcatgt gagcaagcgg tgtgcacacg	1050
gagactcatc gttataattt actatctgcc aagagtagaa agaaaggctg gggatatttg	1110
ggttggcttg gttttgattt tttgcttggt tgtttgtttt gtactaaaac agtattatct	1170
tttgaatata gtagggacat aagtatatac atgttatcca atcaagatgg ctagaatggt	1230
gcctttctga gtgtctaaaa cttgacaccc ctggtaaatac tttcaacaca cttccactgc	1290
ctgcgtaatg aagttttgat tcatttttaa ccaactggaat ttttcaatgc cgtcattttc	1350
agttagatga ttttgcactt tgagattaaa atgccatgac tatttgatta gtcttatttt	1410
tttattttta caggcttata agtctcactg ttggctgtca ttgtgacaaa gtcaaataaa	1470
ccccaagga cgacacacag tatggatcac atattgtttg acattaagct tttgccagaa	1530

Sequence Listing

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aatgttgcat gtgttttacc tcgacttgct aaaatcgatt agcagaaagg catggctaataat 1590
aatgttggtg gtgaaaataa ataaataagt aaacaaaatg aagattgcct gctctctctg 1650
tgcctagcct caaagcggtc atcatatc atacctttaa gattgctata ttttgggtta 1710
ttttcttgac aggagaaaaa gatctaaaga tcttttattt tcatcttttt tggttttctt 1770
ggcatgacta agaagcttaa atgttgataa aatatgacta gttttgaatt tacaccaaga 1830
acttctcaat aaaagaaaat catgaatgct ccacaatttc aacataccac aagagaagtt 1890
aatttcttaa cattgtgttc tatgattatt tgtaagacct tcaccaagtt ctgatatctt 1950
ttaaagacat agttcaaaat tgcttttgaa aatctgtatt cttgaaaata tccttgttgt 2010
gtattaggtt tttaaatacc agctaaagga ttacctcact gagtcatcag taccctccta 2070
ttcagctccc caagatgatg tgtttttgct taccctaaga gaggttttct tcttattttt 2130
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aaagaaaatt taatatgtta tagctgaatc tttttggtta ctttaaactt ttatcataga 2250
ctctgtacat atgttcaaat tagctgcttg cctgatgtgt gtatcatcgg tgggatgaca 2310
gaacaaacat atttatgatc atgaataatg tgctttgtaa aaagatttca agttattagg 2370
aagcatactc tgttttttta tcatgtataa tattccatga tacttttata gaacaattct 2430
ggcttcagga aagtctagaa gcaatatttc ttcaaataaa aggtgtttta actttaaaaa 2490
aaaaaaaaa 2500

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<210> 12
<211> 267
<212> PRT
<213> Homo sapiens

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Sequence Listing

<400> 12

Met Asp Gly Lys Val Asn Gln Pro Arg Leu Thr Ala Asp Ile Asn Trp
 1 5 10 15

Gln Gly Leu Glu Glu Leu His Ser Val Asn Glu Asn Ile Tyr Glu Tyr
 20 25 30

Arg Gln Asn Tyr Arg Leu Ser Leu Val Asp Trp Thr Asn Tyr Leu Lys
 35 40 45

Asp Leu Asp Arg Val Phe Ala Leu Leu Lys Ser His Tyr Glu Gln Asn
 50 55 60

Lys Thr Asn Lys Thr Gln Thr Ala Gln Ser Asp Gly Phe Leu Val Val
 65 70 75 80

Ser Ala Glu His Ala Val Ser Met Glu Met Ala Ser Ala Asp Ser Asp
 85 90 95

Glu Asp Pro Arg His Lys Val Gly Lys Thr Pro His Leu Thr Leu Pro
 100 105 110

Ala Asp Leu Gln Thr Leu His Leu Asn Arg Pro Thr Leu Ser Pro Glu
 115 120 125

Ser Lys Leu Glu Trp Asn Asn Asp Ile Pro Glu Val Asn His Leu Asn
 130 135 140

Ser Glu His Trp Arg Lys Thr Glu Lys Trp Thr Gly His Glu Glu Thr
 145 150 155 160

Asn His Leu Glu Thr Asp Phe Ser Gly Asp Gly Met Thr Glu Leu Glu
 165 170 175

Leu Gly Pro Ser Pro Arg Leu Gln Pro Ile Arg Arg His Pro Lys Glu
 180 185 190

Leu Pro Gln Tyr Gly Gly Pro Gly Lys Asp Ile Phe Glu Asp Gln Leu
 195 200 205

Sequence Listing

Tyr Leu Pro Val His Ser Asp Gly Ile Ser Val His Gln Met Phe Thr
 210 215 220

Met Ala Thr Ala Glu His Arg Ser Asn Ser Ser Ile Ala Gly Lys Met
 225 230 235 240

Leu Thr Lys Val Glu Lys Asn His Glu Lys Glu Lys Ser Gln His Leu
 245 250 255

Glu Gly Ser Ala Ser Ser Ser Leu Ser Ser Asp
 260 265

<210> 13
 <211> 6405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (49)..(1434)
 <223> Gene LBFL305

<400> 13
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 Met Glu Thr
 1

gta cag ctg agg aac ccg ccg cgc cgg cag ctg aaa aag ttg gat gaa 105
 Val Gln Leu Arg Asn Pro Pro Arg Arg Gln Leu Lys Lys Leu Asp Glu
 5 10 15

gat agt tta acc aaa caa cca gaa gaa gta ttt gat gtc tta gag aaa 153
 Asp Ser Leu Thr Lys Gln Pro Glu Glu Val Phe Asp Val Leu Glu Lys
 20 25 30 35

ctt gga gaa ggg tcc tat ggc agc gta tac aaa gct att cat aaa gag 201
 Leu Gly Glu Gly Ser Tyr Gly Ser Val Tyr Lys Ala Ile His Lys Glu

Sequence Listing

40	45	50	
acc ggc cag att gtt gct att aag caa gtt cct gtg gaa tca gac ctc			249
Thr Gly Gln Ile Val Ala Ile Lys Gln Val Pro Val Glu Ser Asp Leu			
55	60	65	
cag gag ata atc aaa gaa atc tct ata atg cag caa tgt gac agc cct			297
Gln Glu Ile Ile Lys Glu Ile Ser Ile Met Gln Gln Cys Asp Ser Pro			
70	75	80	
cat gta gtc aaa tat tac ggc agt tat ttt aag aac aca gac tta tgg			345
His Val Val Lys Tyr Tyr Gly Ser Tyr Phe Lys Asn Thr Asp Leu Trp			
85	90	95	
atc gtt atg gag tac tgt ggg gct ggt tct gta tct gat atc att cga			393
Ile Val Met Glu Tyr Cys Gly Ala Gly Ser Val Ser Asp Ile Ile Arg			
100	105	110	115
tta cga aat aaa acg tta aca gaa gat gaa ata gct aca ata tta caa			441
Leu Arg Asn Lys Thr Leu Thr Glu Asp Glu Ile Ala Thr Ile Leu Gln			
120	125	130	
tca act ctt aag gga ctt gaa tac ctt cat ttt atg aga aaa ata cac			489
Ser Thr Leu Lys Gly Leu Glu Tyr Leu His Phe Met Arg Lys Ile His			
135	140	145	
cga gat atc aag gca gga aat att ttg cta aat aca gaa gga cat gca			537
Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Asn Thr Glu Gly His Ala			
150	155	160	
aaa ctt gca gat ttt ggg gta gca ggt caa ctt aca gat acc atg gcc			585
Lys Leu Ala Asp Phe Gly Val Ala Gly Gln Leu Thr Asp Thr Met Ala			
165	170	175	
aag cgg aat aca gtg ata gga aca cca ttt tgg atg gct cca gaa gtg			633
Lys Arg Asn Thr Val Ile Gly Thr Pro Phe Trp Met Ala Pro Glu Val			
180	185	190	195
att cag gaa att gga tac aac tgt gta gca gac atc tgg tcc ctg gga			681
Ile Gln Glu Ile Gly Tyr Asn Cys Val Ala Asp Ile Trp Ser Leu Gly			

Sequence Listing

200	205	210	
ata act gcc ata gaa atg gct gaa gga aag ccc cct tat gct gat atc			729
Ile Thr Ala Ile Glu Met Ala Glu Gly Lys Pro Pro Tyr Ala Asp Ile			
215	220	225	
cat cca atg agg gca atc ttc atg att cct aca aat cct cct ccc aca			777
His Pro Met Arg Ala Ile Phe Met Ile Pro Thr Asn Pro Pro Pro Thr			
230	235	240	
ttc cga aaa cca gag cta tgg tca gat aac ttt aca gat ttt gtg aaa			825
Phe Arg Lys Pro Glu Leu Trp Ser Asp Asn Phe Thr Asp Phe Val Lys			
245	250	255	
cag tgt ctt gta aag agc cct gag cag agg gcc aca gcc act cag ctc			873
Gln Cys Leu Val Lys Ser Pro Glu Gln Arg Ala Thr Ala Thr Gln Leu			
260	265	270	275
ctg cag cac cca ttt gtc agg agt gcc aaa gga gtg tca ata ctg cga			921
Leu Gln His Pro Phe Val Arg Ser Ala Lys Gly Val Ser Ile Leu Arg			
280	285	290	
gac tta att aat gaa gcc atg gat gtg aaa ctg aaa cgc cag gaa tcc			969
Asp Leu Ile Asn Glu Ala Met Asp Val Lys Leu Lys Arg Gln Glu Ser			
295	300	305	
cag cag cgg gaa gtg gac cag gac gat gaa gaa aac tca gaa gag gat			1017
Gln Gln Arg Glu Val Asp Gln Asp Asp Glu Glu Asn Ser Glu Glu Asp			
310	315	320	
gaa atg gat tct ggc acg atg gtt cga gca gtg ggt gat gag atg ggc			1065
Glu Met Asp Ser Gly Thr Met Val Arg Ala Val Gly Asp Glu Met Gly			
325	330	335	
act gtc cga gta gcc agc acc atg act gat gga gcc aat act atg att			1113
Thr Val Arg Val Ala Ser Thr Met Thr Asp Gly Ala Asn Thr Met Ile			
340	345	350	355
gag cac gat gac acg ttg cca tca caa ctg ggc acc atg gtg atc aat			1161
Glu His Asp Asp Thr Leu Pro Ser Gln Leu Gly Thr Met Val Ile Asn			

Sequence Listing

360	365	370	
gca gag gat gag gaa gag gaa gga act atg aaa aga agg gat gag acc			1209
Ala Glu Asp Glu Glu Glu Gly Thr Met Lys Arg Arg Asp Glu Thr			
375	380	385	
atg cag cct gcg aaa cca tcc ttt ctt gaa tat ttt gaa caa aaa gaa			1257
Met Gln Pro Ala Lys Pro Ser Phe Leu Glu Tyr Phe Glu Gln Lys Glu			
390	395	400	
aag gaa aac cag atc aac agc ttt ggc aag agt gta cct ggt cca ctg			1305
Lys Glu Asn Gln Ile Asn Ser Phe Gly Lys Ser Val Pro Gly Pro Leu			
405	410	415	
aaa aat tct tca gat tgg aaa ata cca cag gat gga gac tac gag ttt			1353
Lys Asn Ser Ser Asp Trp Lys Ile Pro Gln Asp Gly Asp Tyr Glu Phe			
420	425	430	435
aaa act agc caa gaa cag cag tct gga aaa gac ata tgt atc caa aat			1401
Lys Thr Ser Gln Glu Gln Gln Ser Gly Lys Asp Ile Cys Ile Gln Asn			
440	445	450	
tgc cag gga aac ctg ctg tgt aga tac gct ttc , tgagaa accacatgct			1450
Cys Gln Gly Asn Leu Leu Cys Arg Tyr Ala Phe			
455	460		
taagagttgg acagtggagg accttcagaa gaggctcttg gccctggacc ccatgatgga			1510
gcaggagatt gaagagatcc ggcagaagta ccagtccaag cggcagccca tcttgatgc			1570
catagaggct aagaagagac ggcaacaaaa cttctgagca aggccaggct gtgagggccc			1630
cagctccacc caggcttttg gtgaattctg gatggcttgc ctcatgtttg ttagccagca			1690
cttctgctct gtcgtctctc cacagcacct ttgtgaactc aggaatgtgc gccagtggga			1750
agggctctct tgacagtcag cgtgccatct tgatgtgtgt atgtacattg gtcaggtata			1810
ttatctcaaa ggatttatat tggcgctttt aactcagagt tttaaaccctc aggaacagag			1870

Sequence Listing

actcctagtt gagtgatagc tgggaaagtt ttacattgtc tgtttttctt ctcccaatag	1930
ctttcaattg ttctttctgg aagactttta aaaaaatata aatatgcata tatatatata	1990
aattataaat agattcccca cgcagtggtg tggcatctct gtacagggtac agttttaaac	2050
ggtttgcctc ttttctgtaa gattatggta ctgtggaaca tgagggcaga ggacaccggg	2110
aggctgttag ggggtcactg aatcccagga gccaacctcc ccctttgcag ggctgcattt	2170
aaaaattagg tttgggacag ttcttgtacc gtggtttcag ccttgtgtgg tcatcactgg	2230
cttctggagc tattggtgat gtccaaggga aagctttgag agtttatgtt tactctttga	2290
gtcccaggag aagcctggca ccctctttgc aaattggcct ttgctctttc aatgccttc	2350
atccatctcc actctctcaa ctgcctaaag tcacagcaca gatactgcc agtgccttaa	2410
gaggagacat gatctctacc agggactctc agcaaacacg ggactgtgtt cagtccaca	2470
aggaaaagcg tttttgaagc tctcattgtt catgtaaaaa tcatacacgt ggcatgttgc	2530
tccacattcc ttacacacag gggtagaggg gattgctttt gtgaccacg ttcaaatatg	2590
tgactgtttt cttttctctt ttactgctaa gcagcctgga aaggataaat gaatattaga	2650
ctaagatttg tttccagga ggctcaatct gaacacacag aatgtcagag ctggaaggga	2710
ctatagagat catctgatct gatcctcttg tacggatgat cgcaaaactg aggtgtagag	2770
aggggaatgg ccaaaatcac aaagcaagtt agcgtaaga gctgagacta gaattcaggg	2830
tctcactcc caggccaccg aacctgcag ccccttcttt gggggaagag acctgtgtca	2890
gtcttggtta attgttccag ggaaccttgc taacagaaac ttgctcttgc cttggctctt	2950
cagtagatga cctggctgta aagagattcc ctggacgagc cagatcattc agtttcagcg	3010
agtccttgag ctccacaaca tctaccagat atagcagaca agcacccatg gaggcaggtt	3070

Sequence Listing

tcgggcctga agcagatcag agggctttgc aaaagacagc atagagccat cttcctgcaa	3130
ctttacctct ttccctcaga tggggagcca tgactgggtt gcacctcagg atactgtaat	3190
ttgactccat aattgctttt gtcctgaaa cctgggaatc aatggaaagg cagggaatgt	3250
gcctcttctg tggccagatt ctgttatctg caattaaagc aagtttttaa aaaatgcaag	3310
aggcagttgt tagtcttcag ggcttggaac ctgaaatagc tatgtggcgg atacggaaaa	3370
cagaggacaa tttgaggatc ttgctggaat aataaatgac agctaccatt tgttgagcac	3430
ctattatata tcaggcactg agctgggtag gctctaaact tcacaataac cctgtgactt	3490
aactacttta tctccatttt gtagttgaag aaataagttc agagagaaag attccttccc	3550
aaggtcatgc agctagtaaa tgatagaatc aggattcata gcatcactat aggggggtcaa	3610
tatttacaca aaaaaggaaa gtcacaagcc tgtttaaaat gaagtgaacca ccttttcttg	3670
catagactaa ataactcgaa ctggcatttt taggttggaag agacagctga attagtagtt	3730
aagtctgata gccaagtaag ttttaaaaac caaagcatcc aggatgcaca cccctgcacc	3790
atttgctgtg cgaattaata gttctgtctc tctctctctt tcttttttct ttttattctt	3850
tgagatggat tttcgtctct gtcgccagc ctggagtaca atggcacgat cttggctcac	3910
tgcaacctcc gcctcccggg ttcaagcgat tcttctgctg ggattacagc atatgcacc	3970
atgccagat tatttttttg tatttgtagt agagacgggg ttccaccatg tcagtcaggc	4030
tggtcttgaa ctctgacct caggtgatcc accgcctca gcctcccaca ctgctgggat	4090
tacaggcatg agccaccgt cctggcctct ctttcttttt taaacaaaga actttgcact	4150
tggccagaga ggaggagaaa gccattttc tcccttccta agctagatcc aaataaaaga	4210
aagttcagtt tcccccata actattcttg ggtcatgaac ttgatctgg agtttgtttt	4270

Sequence Listing

gtttcaggaa tgtgtgcacc cagcttgctg atccaacaaa gtctattgct taccagtcta	4330
gcttgatgaa gccttttggc cagaagtcaa ttgtttttgg atcagagaaa tttcctgaca	4390
aggtatattt gttttctagt gacagaaagg caaaggaaca agtcctagtt gttgttggtg	4450
ttgttgaata ctaaatttaa gatatgtcag cttgctttca atgagccttg ggcttctgtt	4510
attgcttgag catttgaac tcgagcttcc agagaaattt gaggtcctcg cttgttctct	4570
gccttcaaga aacaatgacc tgattctgtc tttaaaaaaa aaatctcaga attctttttt	4630
tgtttgtgtt tttttttttg agacagagtc tcaactctgtt gccaggctg gagtgcagtg	4690
gcgccatctc ggctcactgc aacctccgcc tcccaggttc aagcaattct cctgcctcag	4750
cctcccaggt agctgccact acagggtgctg caccaccacg cccggctaata ttttgtattt	4810
ttagtagaga cagggtttca ccatattagc cagggtgggtc ttgaactcct gaccttgatga	4870
tccaccgcc tcggcctccc aaagtgtctg gattacaggc gtgagccacc ttgcctggcc	4930
aaaaatctca gaattcttta agactgtttt aattgctcca tcagtaattt tgaagcactt	4990
tccttttttt ttttccctt tttgtccctt tccccagcc accaattgga tggatgaatg	5050
tttgacgggg aagaggaagg gtaggaggat gcatggatga gtggatgagt ggatcgatgg	5110
atgtattgat aaatagatag aaccagtcac ctgaagcaac ttaagaattg tagccttgac	5170
tccttgagac ttagatttc gatccaggaa acatttattt agcacctgcc agatgccaga	5230
aatttatacc atttaaaact cagtaagtct tttaaatatc aggaaggaga gaagcgacat	5290
catgatacat cctatgggta ttaaaaagcc aatagaatat tatgaataat tttatgctaa	5350
taaatttaac aacttcaaca tcataaaca attccttgaa aaataaaaag taccaaaatt	5410
cattcaagaa gaaatagata ccagcctgag caacatggca aaatcccatc tctacaaaac	5470

Sequence Listing

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atcaaaaaaa aaaaattagt cgggcatggt ggtgcacacc tgtaatccca gcttgtcagg      5530
aggctgaagt gggaggatca cctgagccca gggagggtcaa ggatgcagtg agccatggtc      5590
tcaccactgc actctagcct aggtgacaga atgagacccc gtctcaaaaa aaaagaagaa      5650
gtagataatc tgaatagccc tataatctata gaaacttaat agtgctggga gatataggta      5710
ttattatcct cattttacag atgtgaaaat tgaggctcag agaagtaaag tctattgctc      5770
aaggatcatgt ggctagaata tggcagagcc atgattcaga tccaggtcct ctgattctta      5830
ttccagtgtc ctttctagca taccatgttg cctctaaaga ttgcagctcc ttatttacta      5890
gaaaattgtt cctgcccaat ctacatctcc acctcacccc atcttttctt aagcactatg      5950
tttgtgtttt tatcagtatt atattcattg tctttggaat acatgttctt gtttgtgttt      6010
ggaaaaaaaa tctcttttac cagcttgac tcggaccaac ttggaaaaaa aaagcttaaa      6070
tgtttttgct atgtacagtt taaaaatgtg aagttttag cttaaacttt ttgtaagaaa      6130
atctaataac actggcttaa gtgctgactt gaaatgctat ttgtaaggt ttggatgtaa      6190
gtaatcaatt gaggtcagca gtttgtatga gacatagctt cctccattgc cccactcct      6250
tttttctttt ttaagtttga gatgcttcct gtgtttttat gttagaattg ttgttctcct      6310
tcttttcttc ttctataacc tcatcacgtt tgttttaaat aaactgtcct ttggaccaca      6370
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa      6405

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<210> 14

<211> 462

<212> PRT

<213> Homo sapiens

<400> 14

Met Glu Thr Val Gln Leu Arg Asn Pro Pro Arg Arg Gln Leu Lys Lys

Sequence Listing

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20	25	30	
Leu Glu Lys Leu Gly Glu Gly Ser Tyr Gly Ser Val Tyr Lys Ala Ile			
35	40	45	
His Lys Glu Thr Gly Gln Ile Val Ala Ile Lys Gln Val Pro Val Glu			
50	55	60	
Ser Asp Leu Gln Glu Ile Ile Lys Glu Ile Ser Ile Met Gln Gln Cys			
65	70	75	80
Asp Ser Pro His Val Val Lys Tyr Tyr Gly Ser Tyr Phe Lys Asn Thr			
85	90	95	
Asp Leu Trp Ile Val Met Glu Tyr Cys Gly Ala Gly Ser Val Ser Asp			
100	105	110	
Ile Ile Arg Leu Arg Asn Lys Thr Leu Thr Glu Asp Glu Ile Ala Thr			
115	120	125	
Ile Leu Gln Ser Thr Leu Lys Gly Leu Glu Tyr Leu His Phe Met Arg			
130	135	140	
Lys Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Asn Thr Glu			
145	150	155	160
Gly His Ala Lys Leu Ala Asp Phe Gly Val Ala Gly Gln Leu Thr Asp			
165	170	175	
Thr Met Ala Lys Arg Asn Thr Val Ile Gly Thr Pro Phe Trp Met Ala			
180	185	190	
Pro Glu Val Ile Gln Glu Ile Gly Tyr Asn Cys Val Ala Asp Ile Trp			
195	200	205	
Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Lys Pro Pro Tyr			
210	215	220	

Sequence Listing

Ala Asp Ile His Pro Met Arg Ala Ile Phe Met Ile Pro Thr Asn Pro
 225 230 235 240

Pro Pro Thr Phe Arg Lys Pro Glu Leu Trp Ser Asp Asn Phe Thr Asp
 245 250 255

Phe Val Lys Gln Cys Leu Val Lys Ser Pro Glu Gln Arg Ala Thr Ala
 260 265 270

Thr Gln Leu Leu Gln His Pro Phe Val Arg Ser Ala Lys Gly Val Ser
 275 280 285

Ile Leu Arg Asp Leu Ile Asn Glu Ala Met Asp Val Lys Leu Lys Arg
 290 295 300

Gln Glu Ser Gln Gln Arg Glu Val Asp Gln Asp Asp Glu Glu Asn Ser
 305 310 315 320

Glu Glu Asp Glu Met Asp Ser Gly Thr Met Val Arg Ala Val Gly Asp
 325 330 335

Glu Met Gly Thr Val Arg Val Ala Ser Thr Met Thr Asp Gly Ala Asn
 340 345 350

Thr Met Ile Glu His Asp Asp Thr Leu Pro Ser Gln Leu Gly Thr Met
 355 360 365

Val Ile Asn Ala Glu Asp Glu Glu Glu Glu Gly Thr Met Lys Arg Arg
 370 375 380

Asp Glu Thr Met Gln Pro Ala Lys Pro Ser Phe Leu Glu Tyr Phe Glu
 385 390 395 400

Gln Lys Glu Lys Glu Asn Gln Ile Asn Ser Phe Gly Lys Ser Val Pro
 405 410 415

Gly Pro Leu Lys Asn Ser Ser Asp Trp Lys Ile Pro Gln Asp Gly Asp
 420 425 430

Sequence Listing

Tyr Glu Phe Lys Thr Ser Gln Glu Gln Gln Ser Gly Lys Asp Ile Cys
 435 440 445

Ile Gln Asn Cys Gln Gly Asn Leu Leu Cys Arg Tyr Ala Phe
 450 455 460

<210> 15
 <211> 1931
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (43)..(1503)
 <223> Mst1/STK4 gene

<400> 15
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 Met Glu Thr
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 gta'cag ctg agg aac ccg ccg cgc cgg cag ctg aaa aag ttg gat gaa 99
 Val Gln Leu Arg Asn Pro Pro Arg Arg Gln Leu Lys Lys Leu Asp Glu
 5 10 15

 gat agt tta acc aaa caa cca gaa gaa gta ttt gat gtc tta gag aaa 147
 Asp Ser Leu Thr Lys Gln Pro Glu Glu Val Phe Asp Val Leu Glu Lys
 20 25 30 35

 ctt gga gaa ggg tcc tat ggc agc gta tac aaa gct att cat aaa gag 195
 Leu Gly Glu Gly Ser Tyr Gly Ser Val Tyr Lys Ala Ile His Lys Glu
 40 45 50

 acc ggc cag att gtt gct att aag caa gtt cct gtg gaa tca gac ctc 243
 Thr Gly Gln Ile Val Ala Ile Lys Gln Val Pro Val Glu Ser Asp Leu
 55 60 65

Sequence Listing

cag gag ata atc aaa gaa atc tct ata atg cag caa tgt gac agc cct Gln Glu Ile Ile Lys Glu Ile Ser Ile Met Gln Gln Cys Asp Ser Pro 70 75 80	291
cat gta gtc aaa tat tat ggc agt tat ttt aag aac aca gac tta tgg His Val Val Lys Tyr Tyr Gly Ser Tyr Phe Lys Asn Thr Asp Leu Trp 85 90 95	339
atc gtt atg gag tac tgt ggg gct ggt tct gta tct gat atc att cga Ile Val Met Glu Tyr Cys Gly Ala Gly Ser Val Ser Asp Ile Ile Arg 100 105 110 115	387
tta cga aat aaa acg tta aca gaa gat gaa ata gct aca ata tta caa Leu Arg Asn Lys Thr Leu Thr Glu Asp Glu Ile Ala Thr Ile Leu Gln 120 125 130	435
tca act ctt aag gga ctt gaa tac ctt cat ttt atg aga aaa ata cac Ser Thr Leu Lys Gly Leu Glu Tyr Leu His Phe Met Arg Lys Ile His 135 140 145	483
cga gat atc aag gca gga aat att ttg cta aat aca gaa gga cat gca Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Asn Thr Glu Gly His Ala 150 155 160	531
aaa ctt gca gat ttt ggg gta gca ggt caa ctt aca gat acc atg gcc Lys Leu Ala Asp Phe Gly Val Ala Gly Gln Leu Thr Asp Thr Met Ala 165 170 175	579
aag cgg aat aca gtg ata gga aca cca ttt tgg atg gct cca gaa gtg Lys Arg Asn Thr Val Ile Gly Thr Pro Phe Trp Met Ala Pro Glu Val 180 185 190 195	627
att cag gaa att gga tac aac tgt gta gca gac atc tgg tcc ctg gga Ile Gln Glu Ile Gly Tyr Asn Cys Val Ala Asp Ile Trp Ser Leu Gly 200 205 210	675
ata act gcc ata gaa atg gct gaa gga aag ccc cct tat gct gat atc Ile Thr Ala Ile Glu Met Ala Glu Gly Lys Pro Pro Tyr Ala Asp Ile 215 220 225	723

Sequence Listing

cat cca atg agg gca atc ttc atg att cct aca aat cct cct ccc aca His Pro Met Arg Ala Ile Phe Met Ile Pro Thr Asn Pro Pro Pro Thr 230 235 240	771
ttc cga aaa cca gag cta tgg tca gat aac ttt aca gat ttt gtg aaa Phe Arg Lys Pro Glu Leu Trp Ser Asp Asn Phe Thr Asp Phe Val Lys 245 250 255	819
cag tgt ctt gta aag agc cct gag cag agg gcc aca gcc act cag ctc Gln Cys Leu Val Lys Ser Pro Glu Gln Arg Ala Thr Ala Thr Gln Leu 260 265 270 275	867
ctg cag cac cca . ttt gtc agg agt gcc aaa gga gtg tca ata ctg cga Leu Gln His Pro Phe Val Arg Ser Ala Lys Gly Val Ser Ile Leu Arg 280 285 290	915
gac tta att aat gaa gcc atg gat gtg aaa ctg aaa cgc cag gaa tcc Asp Leu Ile Asn Glu Ala Met Asp Val Lys Leu Lys Arg Gln Glu Ser 295 300 305	963
cag cag cgg gaa gtg gac cag gac gat gaa gaa aac tca gaa gag gat Gln Gln Arg Glu Val Asp Gln Asp Asp Glu Glu Asn Ser Glu Glu Asp 310 315 320	1011
gaa atg gat tct ggc acg atg gtt cga gca gtg ggt gat gag atg ggc Glu Met Asp Ser Gly Thr Met Val Arg Ala Val Gly Asp Glu Met Gly 325 330 335	1059
act gtc cga gta gcc agc acc atg act gat gga gcc aat act atg att Thr Val Arg Val Ala Ser Thr Met Thr Asp Gly Ala Asn Thr Met Ile 340 345 350 355	1107
gag cac gat gac acg ttg cca tca caa ctg ggc acc atg gtg atc aat Glu His Asp Asp Thr Leu Pro Ser Gln Leu Gly Thr Met Val Ile Asn 360 365 370	1155
gca gag gat gag gaa gag gaa gga act atg aaa aga agg gat gag acc Ala Glu Asp Glu Glu Glu Glu Gly Thr Met Lys Arg Arg Asp Glu Thr 375 380 385	1203

Sequence Listing

atg cag cct gcg aaa cca tcc ttt ctt gaa tat ttt gaa caa aaa gaa	1251
Met Gln Pro Ala Lys Pro Ser Phe Leu Glu Tyr Phe Glu Gln Lys Glu	
390 395 400	
aag gaa aac cag atc aac agc ttt ggc aag agt gta cct ggt cca ctg	1299
Lys Glu Asn Gln Ile Asn Ser Phe Gly Lys Ser Val Pro Gly Pro Leu	
405 410 415	
aaa aat tct tca gat tgg aaa ata cca cag gat gga gac tac gag ttt	1347
Lys Asn Ser Ser Asp Trp Lys Ile Pro Gln Asp Gly Asp Tyr Glu Phe	
420 425 430 435	
ctt aag agt tgg aca gtg gag gac ctt cag aag agg ctc ttg gcc ctg	1395
Leu Lys Ser Trp Thr Val Glu Asp Leu Gln Lys Arg Leu Leu Ala Leu	
440 445 450	
gac ccc atg atg gag cag gag att gaa gag atc cgg cag aag tac cag	1443
Asp Pro Met Met Glu Gln Glu Ile Glu Glu Ile Arg Gln Lys Tyr Gln	
455 460 465	
tcc aag cgg cag ccc atc ctg gat gcc ata gag gct aag aag aga cgg	1491
Ser Lys Arg Gln Pro Ile Leu Asp Ala Ile Glu Ala Lys Lys Arg Arg	
470 475 480	
caa caa aac ttc tgagcaa ggccaggctg tgaggggcccc agtccacccc	1540
Gln Gln Asn Phe	
485	
aggctttggg tgaattctgg atggcttgcc tcatgtttgt tagccagcac ttctgctctg	1600
tcgtctctcc acagcacctt tgtgaaactca ggaatgtgcy ccagtgggaa gggctctctt	1660
gacagtcagc gtgccatctt gatgtgtgta tgtacattgg tcaggtatat tatctcaaag	1720
gatttatatt ggcgctttta actcagagtt ttaaacccca ggaacagaga ctcctagttg	1780
agtgatagct gggaaagttt tacattgtct gtttttcttc tcccaatagc tttcaattgt	1840
tctttctgga agacttttaa aaaaatataa atatgcatat atatataata attataaata	1900

Sequence Listing

gattccccac gcaggtgggtg gcatctctgt a

1931

<210> 16

<211> 487

<212> PRT

<213> Homo sapiens

<400> 16

Met Glu Thr Val Gln Leu Arg Asn Pro Pro Arg Arg Gln Leu Lys Lys

1 5 10 15

Leu Asp Glu Asp Ser Leu Thr Lys Gln Pro Glu Glu Val Phe Asp Val

20 25 30

Leu Glu Lys Leu Gly Glu Gly Ser Tyr Gly Ser Val Tyr Lys Ala Ile

35 40 45

His Lys Glu Thr Gly Gln Ile Val Ala Ile Lys Gln Val Pro Val Glu

50 55 60

Ser Asp Leu Gln Glu Ile Ile Lys Glu Ile Ser Ile Met Gln Gln Cys

65 70 75 80

Asp Ser Pro His Val Val Lys Tyr Tyr Gly Ser Tyr Phe Lys Asn Thr

85 90 95

Asp Leu Trp Ile Val Met Glu Tyr Cys Gly Ala Gly Ser Val Ser Asp

100 105 110

Ile Ile Arg Leu Arg Asn Lys Thr Leu Thr Glu Asp Glu Ile Ala Thr

115 120 125

Ile Leu Gln Ser Thr Leu Lys Gly Leu Glu Tyr Leu His Phe Met Arg

130 135 140

Lys Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Asn Thr Glu

145 150 155 160

Sequence Listing

Gly His Ala Lys Leu Ala Asp Phe Gly Val Ala Gly Gln Leu Thr Asp
 165 170 175

Thr Met Ala Lys Arg Asn Thr Val Ile Gly Thr Pro Phe Trp Met Ala
 180 185 190

Pro Glu Val Ile Gln Glu Ile Gly Tyr Asn Cys Val Ala Asp Ile Trp
 195 200 205

Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Lys Pro Pro Tyr
 210 215 220

Ala Asp Ile His Pro Met Arg Ala Ile Phe Met Ile Pro Thr Asn Pro
 225 230 235 240

Pro Pro Thr Phe Arg Lys Pro Glu Leu Trp Ser Asp Asn Phe Thr Asp
 245 250 255

Phe Val Lys Gln Cys Leu Val Lys Ser Pro Glu Gln Arg Ala Thr Ala
 260 265 270

Thr Gln Leu Leu Gln His Pro Phe Val Arg Ser Ala Lys Gly Val Ser
 275 280 285

Ile Leu Arg Asp Leu Ile Asn Glu Ala Met Asp Val Lys Leu Lys Arg
 290 295 300

Gln Glu Ser Gln Gln Arg Glu Val Asp Gln Asp Asp Glu Glu Asn Ser
 305 310 315 320

Glu Glu Asp Glu Met Asp Ser Gly Thr Met Val Arg Ala Val Gly Asp
 325 330 335

Glu Met Gly Thr Val Arg Val Ala Ser Thr Met Thr Asp Gly Ala Asn
 340 345 350

Thr Met Ile Glu His Asp Asp Thr Leu Pro Ser Gln Leu Gly Thr Met
 355 360 365

Val Ile Asn Ala Glu Asp Glu Glu Glu Glu Gly Thr Met Lys Arg Arg

Sequence Listing

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370          375          380
Asp Glu Thr Met Gln Pro Ala Lys Pro Ser Phe Leu Glu Tyr Phe Glu
385          390          395          400
Gln Lys Glu Lys Glu Asn Gln Ile Asn Ser Phe Gly Lys Ser Val Pro
          405          410          415
Gly Pro Leu Lys Asn Ser Ser Asp Trp Lys Ile Pro Gln Asp Gly Asp
          420          425          430
Tyr Glu Phe Leu Lys Ser Trp Thr Val Glu Asp Leu Gln Lys Arg Leu
          435          440          445
Leu Ala Leu Asp Pro Met Met Glu Gln Glu Ile Glu Glu Ile Arg Gln
          450          455          460
Lys Tyr Gln Ser Lys Arg Gln Pro Ile Leu Asp Ala Ile Glu Ala Lys
465          470          475          480
Lys Arg Arg Gln Gln Asn Phe
          485

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<210> 17
<211> 1299
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (75)..(572)
<223> Clone no. LBFL306-EF3

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<400> 17
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tccggtgacg gacc      atg tcg gcg gcg gga gcg ggc gcg ggc gta gag 107
      Met Ser Ala Ala Gly Ala Gly Ala Gly Val Glu

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Sequence Listing

1	5	10	
gcg ggc ttc tcc agc gag gag ctg ctc tcg ctc cgt ttc ccg .ctg cac			155
Ala Gly Phe Ser Ser Glu Glu Leu Leu Ser Leu Arg Phe Pro Leu His			
15	20	25	
cgc gcc tgc cgc gac ggg gac ctg gcc acg ctc tgc tcg ctg ctg cag			203
Arg Ala Cys Arg Asp Gly Asp Leu Ala Thr Leu Cys Ser Leu Leu Gln			
30	35	40	
cag aca ccc cac gcc cac ctg gcc tct gag gac tcc ttc tat ggc tgg			251
Gln Thr Pro His Ala His Leu Ala Ser Glu Asp Ser Phe Tyr Gly Trp			
45	50	55	
acg ccc gtg cac tgg gcc gcg cat ttc ggc aag ttg gag tgc tta gtg			299
Thr Pro Val His Trp Ala Ala His Phe Gly Lys Leu Glu Cys Leu Val			
60	65	70	75
cag ttg gtg aga gcg gga gcc aca ctc aac gtc tcc acc aca cgg tac			347
Gln Leu Val Arg Ala Gly Ala Thr Leu Asn Val Ser Thr Thr Arg Tyr			
80	85	90	
gcg cag acg cca gcc cac att gca gcc ttt ggg gga cat cct cag tgc			395
Ala Gln Thr Pro Ala His Ile Ala Ala Phe Gly Gly His Pro Gln Cys			
95	100	105	
ctg gtc tgg ctg att caa gca gga gcc aac att aac aaa ccg gat tgt			443
Leu Val Trp Leu Ile Gln Ala Gly Ala Asn Ile Asn Lys Pro Asp Cys			
110	115	120	
gag ggt gaa act ccc att cac aag gca gct cgc tct ggg agc cta gaa			491
Glu Gly Glu Thr Pro Ile His Lys Ala Ala Arg Ser Gly Ser Leu Glu			
125	130	135	
tgc atc agt gcc ctt gtg gcg aat ggg gct cac gtc gat aac ccc aag			539
Cys Ile Ser Ala Leu Val Ala Asn Gly Ala His Val Asp Asn Pro Lys			
140	145	150	155
aaa ggc atc agg gtt ctg gag tgg ttg ttt gag tgacacag cacaaggcct			590
Lys Gly Ile Arg Val Leu Glu Trp Leu Phe Glu			

Sequence Listing

160

165

```

tgatttcac atgcttttgc tgtggatgta gtgtagcttg ctgaacaggt ttatttcaca      650
gagcagtgtg cattcttgtc ttccagggga acttcaacat ggagttactt ttgatccctc      710
agttttaatt cagtgtctaa agcctgagaa atgccagtg cctgacagca gcagacattg      770
cacaaacca gggtttccaa gagtgtgcc agtttctctt gaacctccag aattgtcatc      830
tgaaccatth ctataacaat ggcattctaa atgggggtca tcagaatgta tttcctaata      890
atattagtgt gggaacaaat cgaagagat gcttggaaga ctcaagac tttggagtaa      950
agaaagctag aactgaaggt gagaccgctt tgcgggtggg aagagcacac ttatttttcc     1010
tttctgtaat atgttttctt tttatggctg agcgcacctt cgagatgaga ccttcacttc     1070
agggtgtaat gcgcctggtg gattgtgcgg tgacggtgga gatttctcct gtactgccac     1130
tgcaagatg ggacacttaa caaaggga tgtgaggga atactgatgg cccaagtgtg     1190
aatgtctatg tggaactttt tgagcaccca tgtttacctg ccgtgaatta gattttttaa     1250
ttgtgttat ctgtttgaaa tatatctatt aaagaaaaaa aaaaaaaaaa     1299

```

<210> 18

<211> 166

<212> PRT

<213> Homo sapiens

<400> 18

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Met Ser Ala Ala Gly Ala Gly Val Glu Ala Gly Phe Ser Ser
  1             5             10             15

```

```

Glu Glu Leu Leu Ser Leu Arg Phe Pro Leu His Arg Ala Cys Arg Asp
      20             25             30

```

```

Gly Asp Leu Ala Thr Leu Cys Ser Leu Leu Gln Gln Thr Pro His Ala

```

Sequence Listing

```

      35              40              45
His Leu Ala Ser Glu Asp Ser Phe Tyr Gly Trp Thr Pro Val His Trp
  50              55              60
Ala Ala His Phe Gly Lys Leu Glu Cys Leu Val Gln Leu Val Arg Ala
  65              70              75              80
Gly Ala Thr Leu Asn Val Ser Thr Thr Arg Tyr Ala Gln Thr Pro Ala
      85              90              95
His Ile Ala Ala Phe Gly Gly His Pro Gln Cys Leu Val Trp Leu Ile
      100              105              110
Gln Ala Gly Ala Asn Ile Asn Lys Pro Asp Cys Glu Gly Glu Thr Pro
      115              120              125
Ile His Lys Ala Ala Arg Ser Gly Ser Leu Glu Cys Ile Ser Ala Leu
      130              135              140
Val Ala Asn Gly Ala His Val Asp Asn Pro Lys Lys Gly Ile Arg Val
      145              150              155              160
Leu Glu Trp Leu Phe Glu
      165

```

```

<210>    19
<211>    2451
<212>    DNA
<213>    Homo sapiens

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<220>
<221>    CDS
<222>    (78)..(1337)
<223>    Clone no. LBFL306-GC7

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<400>    19
gctgcggcgg cggtctctcg agtcctcccc gacgcgtcct ctaggccagc gagccccgcg

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60

Sequence Listing

ctctccggtg acggacc	atg tcg gcg gcg gga gcg ggc gcg ggc gta gag	110
	Met Ser Ala Ala Gly Ala Gly Ala Gly Val Glu	
	1 5 10	
gcg ggc ttc tcc agc gag gag ctg ctc tcg ctc cgt ttc ccg ctg cac		158
Ala Gly Phe Ser Ser Glu Glu Leu Leu Ser Leu Arg Phe Pro Leu His		
	15 20 25	
cgc gcc tgc cgc gac ggg gac ctg gcc acg ctc tgc tcg ctg ctg cag		206
Arg Ala Cys Arg Asp Gly Asp Leu Ala Thr Leu Cys Ser Leu Leu Gln		
	30 35 40	
cag aca ccc cac gcc cac ctg gcc tct gag gac tcc ttc tat ggc tgg		254
Gln Thr Pro His Ala His Leu Ala Ser Glu Asp Ser Phe Tyr Gly Trp		
	45 50 55	
acg ccc gtg cac tgg gcc gcg cat ttc ggc aag ttg gag tgc tta gtg		302
Thr Pro Val His Trp Ala Ala His Phe Gly Lys Leu Glu Cys Leu Val		
	60 65 70 75	
cag ttg gtg aga gcg gga gcc aca ctc aac gtc tcc acc aca cgg tac		350
Gln Leu Val Arg Ala Gly Ala Thr Leu Asn Val Ser Thr Thr Arg Tyr		
	80 85 90	
gcg cag acg cca gcc cac att gca gcc ttt ggg gga cat cct cag tgc		398
Ala Gln Thr Pro Ala His Ile Ala Ala Phe Gly Gly His Pro Gln Cys		
	95 100 105	
ctg gtc tgg ctg att caa gca gga gcc aac att aac aaa ccg gat tgt		446
Leu Val Trp Leu Ile Gln Ala Gly Ala Asn Ile Asn Lys Pro Asp Cys		
	110 115 120	
gag ggt gaa act ccc att cac aag gca gct cgc tct ggg agc cta gaa		494
Glu Gly Glu Thr Pro Ile His Lys Ala Ala Arg Ser Gly Ser Leu Glu		
	125 130 135	
tgc atc agt gcc ctt gtg gcg aat ggg gct cac gtc gac ctg aga aat		542
Cys Ile Ser Ala Leu Val Ala Asn Gly Ala His Val Asp Leu Arg Asn		
	140 145 150 155	

Sequence Listing

gcc agt ggc ctg aca gca gca gac att gca caa acc cag ggt ttc caa	590
Ala Ser Gly Leu Thr Ala Ala Asp Ile Ala Gln Thr Gln Gly Phe Gln	
160 165 170	
gag tgt gcc cag ttt ctc ttg aac ctc cag aat tgt cat ctg aac cat	638
Glu Cys Ala Gln Phe Leu Leu Asn Leu Gln Asn Cys His Leu Asn His	
175 180 185	
ttc tat aac aat ggc atc tta aat ggg ggt cat cag aat gta ttt cct	686
Phe Tyr Asn Asn Gly Ile Leu Asn Gly Gly His Gln Asn Val Phe Pro	
190 195 200	
aat cat att agt gtg gga aca aat cga aag aga tgc ttg gaa gac tca	734
Asn His Ile Ser Val Gly Thr Asn Arg Lys Arg Cys Leu Glu Asp Ser	
205 210 215	
gaa gac ttt gga gta aag aaa gct aga act gaa gct caa agc ttg gat	782
Glu Asp Phe Gly Val Lys Lys Ala Arg Thr Glu Ala Gln Ser Leu Asp	
220 225 230 235	
tct gcc gtg cca ctc acg aat ggc gac aca gaa gac gat gct gac aaa	830
Ser Ala Val Pro Leu Thr Asn Gly Asp Thr Glu Asp Asp Ala Asp Lys	
240 245 250	
atg cac gtt gat agg gag ttt gct gtt gta aca gat atg aaa aac agt	878
Met His Val Asp Arg Glu Phe Ala Val Val Thr Asp Met Lys Asn Ser	
255 260 265	
agc tcc gta tcg aat aca ttg aca aat gga tgt gtc atc aat gga cat	926
Ser Ser Val Ser Asn Thr Leu Thr Asn Gly Cys Val Ile Asn Gly His	
270 275 280	
ttg gac ttc ccc tcc acg acc ccg ctc agt ggg atg gaa agc agg aat	974
Leu Asp Phe Pro Ser Thr Thr Pro Leu Ser Gly Met Glu Ser Arg Asn	
285 290 295	
ggc cag tgc ttg aca gga act aac gga att agc agt gga tta gcc cca	1022
Gly Gln Cys Leu Thr Gly Thr Asn Gly Ile Ser Ser Gly Leu Ala Pro	
300 305 310 315	

Sequence Listing

gga cag ccg ttt ccg agt agc cag ggt tct ctc tgc att agt ggg act Gly Gln Pro Phe Pro Ser Ser Gln Gly Ser Leu Cys Ile Ser Gly Thr 320 325 330	1070
gag gag cca gag aag acc ctg aga gct aac cct gag ttg tgc ggt tct Glu Glu Pro Glu Lys Thr Leu Arg Ala Asn Pro Glu Leu Cys Gly Ser 335 340 345	1118
ctg cac ctg aac ggg agt cca agt agc tgc ata gcc agt agg cct tcc Leu His Leu Asn Gly Ser Pro Ser Ser Cys Ile Ala Ser Arg Pro Ser 350 355 360	1166
tgg gtg gaa gac att ggg gat aac ctg tac tat gga cac tac cac ggg Trp Val Glu Asp Ile Gly Asp Asn Leu Tyr Tyr Gly His Tyr His Gly 365 370 375	1214
ttt ggg gac act gct gaa agc atc cca gaa ctg aac agt gtg gtc gag Phe Gly Asp Thr Ala Glu Ser Ile Pro Glu Leu Asn Ser Val Val Glu 380 385 390 395	1262
cat tcc aag tcc gtg aag gtg cag gag cgg tac gac agt gcc gtg ctg His Ser Lys Ser Val Lys Val Gln Glu Arg Tyr Asp Ser Ala Val Leu 400 405 410	1310
ggc acc atg cac ctg cac cac ggc tcc tag agacgctgac ctggctctcg Gly Thr Met His Leu His His Gly Ser 415 420	1360
gaaacgcagg agtccttcct ggtagccagc tcagaatacc catgtagcag caacttgaac	1420
gaatgtcaca acttgtacgt tttttatata cttcaacttt ctgaaaaagt aaacttcgac	1480
aagttccag caactgcttg tttgtgcatg agtagggctt actaagtgca tagatgtttc	1540
tacagtgagg tgtccttttt ataagggtgca cttttggagt tcttctgatg ccaatctcaa	1600
cattgtcttt ttaatactgt caccagatat tgccattttt ctttttgta aaagattata	1660
tgatcaagat aaattggggg ggtaaatacag gtgcctggta atttatctct ttgcacatgg	1720

Sequence Listing

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gcatcatttt aaaaagcttg cttccactct tttctgtaga atttgacgga acacagctat      1780
ttccctatgc aaggtaacgc cttacaaaga tttctgcagt gatttgtgtg aagaagagaa      1840
cgtttgtctt tttcaatgaa gctttgcaga tcacatgtg gttgaagggt ttagttgtgg      1900
acacagtggg cctccttaa tgatgaagat cactgccttg ggcttcatgg aaaacaggcc      1960
cagcctgggg ctgcgtttgg atttattgtt tttattccac acttcctact tggctctctg      2020
aagttttacc acatgtaaca gattccttta tatgtagtgg aaatcactat ttgtagaaac      2080
tgtcagggtca aaatatttaa ctgactgttg acatgtattt tcttttttcc ttgtttttgt      2140
tttttagggg tttctgcttt aagatatata ccactatgta tatccagtta actgagagaa      2200
ttttgactct cttaataaaa ctgcattaag tttttgattt tgtagaaatt agcttttctc      2260
taggcaacta gtggttatac tctgcaaata ttgtaatgaa tttttacttt tttgattttt      2320
gtaataaaaa ttggtgcaga taaaatgtca aatgaacaaa ccagtgttct aagagtgtta      2380
ctaacatttt gttctaaaac tgtccttcac aaattgaata aaaaactctc acactcaaaa      2440
aaaaaaaaaa a                                                                2451

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<210> 20

<211> 420

<212> PRT

<213> Homo sapiens

<400> 20

Met Ser Ala Ala Gly Ala Gly Ala Gly Val Glu Ala Gly Phe Ser Ser

1

5

10

15

Glu Glu Leu Leu Ser Leu Arg Phe Pro Leu His Arg Ala Cys Arg Asp

20

25

30

Sequence Listing

Gly Asp Leu Ala Thr Leu Cys Ser Leu Leu Gln Gln Thr Pro His Ala
 35 40 45

His Leu Ala Ser Glu Asp Ser Phe Tyr Gly Trp Thr Pro Val His Trp
 50 55 60

Ala Ala His Phe Gly Lys Leu Glu Cys Leu Val Gln Leu Val Arg Ala
 65 70 75 80

Gly Ala Thr Leu Asn Val Ser Thr Thr Arg Tyr Ala Gln Thr Pro Ala
 85 90 95

His Ile Ala Ala Phe Gly Gly His Pro Gln Cys Leu Val Trp Leu Ile
 100 105 110

Gln Ala Gly Ala Asn Ile Asn Lys Pro Asp Cys Glu Gly Glu Thr Pro
 115 120 125

Ile His Lys Ala Ala Arg Ser Gly Ser Leu Glu Cys Ile Ser Ala Leu
 130 135 140

Val Ala Asn Gly Ala His Val Asp Leu Arg Asn Ala Ser Gly Leu Thr
 145 150 155 160

Ala Ala Asp Ile Ala Gln Thr Gln Gly Phe Gln Glu Cys Ala Gln Phe
 165 170 175

Leu Leu Asn Leu Gln Asn Cys His Leu Asn His Phe Tyr Asn Asn Gly
 180 185 190

Ile Leu Asn Gly Gly His Gln Asn Val Phe Pro Asn His Ile Ser Val
 195 200 205

Gly Thr Asn Arg Lys Arg Cys Leu Glu Asp Ser Glu Asp Phe Gly Val
 210 215 220

Lys Lys Ala Arg Thr Glu Ala Gln Ser Leu Asp Ser Ala Val Pro Leu
 225 230 235 240

Thr Asn Gly Asp Thr Glu Asp Asp Ala Asp Lys Met His Val Asp Arg

Sequence Listing

245	250	255
Glu Phe Ala Val Val Thr Asp Met Lys Asn Ser Ser Ser Val Ser Asn		
260	265	270
Thr Leu Thr Asn Gly Cys Val Ile Asn Gly His Leu Asp Phe Pro Ser		
275	280	285
Thr Thr Pro Leu Ser Gly Met Glu Ser Arg Asn Gly Gln Cys Leu Thr		
290	295	300
Gly Thr Asn Gly Ile Ser Ser Gly Leu Ala Pro Gly Gln Pro Phe Pro		
305	310	315
Ser Ser Gln Gly Ser Leu Cys Ile Ser Gly Thr Glu Glu Pro Glu Lys		
325	330	335
Thr Leu Arg Ala Asn Pro Glu Leu Cys Gly Ser Leu His Leu Asn Gly		
340	345	350
Ser Pro Ser Ser Cys Ile Ala Ser Arg Pro Ser Trp Val Glu Asp Ile		
355	360	365
Gly Asp Asn Leu Tyr Tyr Gly His Tyr His Gly Phe Gly Asp Thr Ala		
370	375	380
Glu Ser Ile Pro Glu Leu Asn Ser Val Val Glu His Ser Lys Ser Val		
385	390	395
Lys Val Gln Glu Arg Tyr Asp Ser Ala Val Leu Gly Thr Met His Leu		
405	410	415
His His Gly Ser		
420		

<210> 21
 <211> 1194
 <212> DNA
 <213> Homo sapiens

Sequence Listing

<220>

<221> CDS

<222> (78)..(737)

<223> Clone no. LBFL-306-GE2

<400> 21

gctgcgggcg cggtttctcg agtcctcccc gacgcgtcct ctaggccagc gagccccgcg 60

ctctccggtg acggacc atg tcg gcg gcg gga gcg ggc gcg ggc gta gag 110
 Met Ser Ala Ala Gly Ala Gly Ala Gly Val Glu
 1 5 10

gcg ggc ttc tcc agc gag gag ctg ctc tcg ctc cgt ttc ccg ctg cac 158
 Ala Gly Phe Ser Ser Glu Glu Leu Leu Ser Leu Arg Phe Pro Leu His
 15 20 25

cgc gcc tgc cgc gac ggg gac ctg gcc acg ctc tgc tcg ctg ctg cag 206
 Arg Ala Cys Arg Asp Gly Asp Leu Ala Thr Leu Cys Ser Leu Leu Gln
 30 35 40

cag aca ccc cac gcc cac ctg gcc tct gag gac tcc ttc tat ggc tgg 254
 Gln Thr Pro His Ala His Leu Ala Ser Glu Asp Ser Phe Tyr Gly Trp
 45 50 55

acg ccc gtg cac tgg gcc gcg cat ttc ggc aag ttg gag tgc tta gtg 302
 Thr Pro Val His Trp Ala Ala His Phe Gly Lys Leu Glu Cys Leu Val
 60 65 70 75

cag ttg gtg aga gcg gga gcc aca ctc aac gtc tcc acc aca cgg tac 350
 Gln Leu Val Arg Ala Gly Ala Thr Leu Asn Val Ser Thr Thr Arg Tyr
 80 85 90

gcg cag acg cca gcc cac att gca gcc ttt ggg gga cat cct cag tgc 398
 Ala Gln Thr Pro Ala His Ile Ala Ala Phe Gly Gly His Pro Gln Cys
 95 100 105

ctg gtc tgg ctg att caa gca gga gcc aac att aac aaa ccg gat tgt 446
 Leu Val Trp Leu Ile Gln Ala Gly Ala Asn Ile Asn Lys Pro Asp Cys

Sequence Listing

110	115	120	
gag ggt gaa act ccc att cac aag gca gct cgc tct ggg agc cta gaa			494
Glu Gly Glu Thr Pro Ile His Lys Ala Ala Arg Ser Gly Ser Leu Glu			
125	130	135	
tgc atc agt gcc ctt gtg gcg aat ggg gct cac gtc gag ttt att tca			542
Cys Ile Ser Ala Leu Val Ala Asn Gly Ala His Val Glu Phe Ile Ser			
140	145	150	155
cag agc agt gta cat tct tgt ctt cca ggg gaa ctt caa cat gga gtt			590
Gln Ser Ser Val His Ser Cys Leu Pro Gly Glu Leu Gln His Gly Val			
160	165	170	
act ttt gat ccc tca gtt tta att cag tgt cta aag cct gag aaa tgc			638
Thr Phe Asp Pro Ser Val Leu Ile Gln Cys Leu Lys Pro Glu Lys Cys			
175	180	185	
cag tgg cct gac agc agc aga cat tgc aca aac cca ggg ttt cca aga			686
Gln Trp Pro Asp Ser Ser Arg His Cys Thr Asn Pro Gly Phe Pro Arg			
190	195	200	
gtg tgc cca gtt tct ctt gaa cct cca gaa ttg tca tct gaa cca ttt			734
Val Cys Pro Val Ser Leu Glu Pro Pro Glu Leu Ser Ser Glu Pro Phe			
205	210	215	
cta taa caatggcatc ttaaattgggg gtcattcagaa tgtatttcct aatcatatta			790
Leu			
220			
gtgtgggaac aaatcgaaag agatgcttgg aagactcaga agactttgga gtaaagaaag			850
ctagaactga aggtgagacc gctttgcggg tgggaagagc acacttattt ttctttctg			910
taatatgttt tctttttatg gctgagcgca ccttcgagat gagaccttca cttcaggtgg			970
taatgcgcct ggtggattgt gcggtgacgg tggagatttc tcctgtactg ccaactgcgaa			1030
gatgggacac ttaacaaaag ggaatgtgag ggaaatactg atggcccaag tgtaaatgtc			1090

Sequence Listing

tatgtggaac tttttgagca cccatgttta cctgccgtga attagatttt ttaatttgtt 1150

gtatctgttt gaaatatatc tattaaagaa aaaaaaaaaa aaaa 1194

<210> 22

<211> 220

<212> PRT

<213> Homo sapiens

<400> 22

Met Ser Ala Ala Gly Ala Gly Ala Gly Val Glu Ala Gly Phe Ser Ser
1 5 10 15

Glu Glu Leu Leu Ser Leu Arg Phe Pro Leu His Arg Ala Cys Arg Asp
20 25 30

Gly Asp Leu Ala Thr Leu Cys Ser Leu Leu Gln Gln Thr Pro His Ala
35 40 45

His Leu Ala Ser Glu Asp Ser Phe Tyr Gly Trp Thr Pro Val His Trp
50 55 60

Ala Ala His Phe Gly Lys Leu Glu Cys Leu Val Gln Leu Val Arg Ala
65 70 75 80

Gly Ala Thr Leu Asn Val Ser Thr Thr Arg Tyr Ala Gln Thr Pro Ala
85 90 95

His Ile Ala Ala Phe Gly Gly His Pro Gln Cys Leu Val Trp Leu Ile
100 105 110

Gln Ala Gly Ala Asn Ile Asn Lys Pro Asp Cys Glu Gly Glu Thr Pro
115 120 125

Ile His Lys Ala Ala Arg Ser Gly Ser Leu Glu Cys Ile Ser Ala Leu
130 135 140

Val Ala Asn Gly Ala His Val Glu Phe Ile Ser Gln Ser Ser Val His
145 150 155 160

Sequence Listing

Ser Cys Leu Pro Gly Glu Leu Gln His Gly Val Thr Phe Asp Pro Ser
165 170 175

Val Leu Ile Gln Cys Leu Lys Pro Glu Lys Cys Gln Trp Pro Asp Ser
180 185 190

Ser Arg His Cys Thr Asn Pro Gly Phe Pro Arg Val Cys Pro Val Ser
195 200 205

Leu Glu Pro Pro Glu Leu Ser Ser Glu Pro Phe Leu
210 215 220